IN THE CLAIMS

Please amend the claims as shown below:

Claims 1-44 (Cancelled)

Claim 45 (Currently Amended): The method of Claim [[1]] 46, wherein the starting mixture of nucleic acids contains nucleic acids comprising sequences SEQ ID NO:1, SEQ ID NO:2, or a fragment of these sequences having at least 8 contiguous nucleotides ~~of these sequences~~.

Claim 46 (Currently Amended): A method for identifying an aptamer for a membrane tyrosine kinase receptor protein (RPTK), comprising:

(a) contacting a mixture of nucleic acids with C_N cells that do not express an active tyrosine kinase receptor protein;

(b) recovering a first subset S1 of nucleic acids which do not bind to the C_N cells in step (a);

(c) bringing said first subset S1 of nucleic acids into contact with C_i cells which express a tyrosine kinase receptor protein that is mutated in its intracellular part;

(d) recovering a second subset S2 of nucleic acids which do not bind to the C_i cells in step (c);

(e) bringing the second subset S2 of nucleic acids into contact with C_{Te} cells;

(f) recovering a third subset S3 of nucleic acids which bind to said C_{Te} cells; and

(g) identifying a nucleic acid in the third subset S3 that binds to an active tyrosine kinase receptor protein, optionally after amplification of S3;

wherein C_N cells, C_i cells, and C_{Te} cells are each of the same cell type but where C_i cells and C_{Te} cells respectively contain mutations in their intracellular or extracellular domains;

wherein C_N cells, C_i cells, and C_{Te} cells express a Ret receptor protein in non-active form, containing an intracellular mutation, or containing an extracellular mutation, respectively.

Claim 47 (Cancelled)

Claim 48 (New): The method of claim 46, wherein the starting mixture of nucleic acids contains nucleic acids comprising sequences SEQ ID NO:1 or a fragment of SEQ ID NO: 1 having at least 8 contiguous nucleotides.

Claim 49 (New): The method of claim 46, wherein the starting mixture of nucleic acids contains nucleic acids comprising sequences SEQ ID NO:2 or a fragment of SEQ ID NO: 2 having at least 8 contiguous nucleotides.